



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo
- (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/586,594
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-162
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCCTCTCTG	60
CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG TTGCTTTGGG	120
AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GAACTGGCT	180
TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG	240
ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC	300
AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT AGATGATTCTG	360
CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGGA	420
TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACCTCACT ACGCTCTTCT GATGTATTTG	480
GAAATCACAT CTGCCGGTGT GAGTTTTTTCAG TCACCTCTGA TGTCCTGCA GCCCATGCTT	540
GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA TGGTAATTTA	600
AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT	660
TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG	720
GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT	780
GGTTCAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG	840
TATTTTCCAC CCAAATTTCT GACTAGTGTT GGATCGAATG CTTCTTTTCA TTGCATCTAC	900
AAAAACGAAA ACCAGATTAT CTCCTCAAAA CAGATAGTTT GGTGGAGGAA TCTAGCTGAG	960
AAAATCCCTG AGATACAGTA CAGCATTGTG AGTGACCGAG TTAGCAAAGT TACCTTCTCC	1020
AACCTGAAAG CCACCAGACC TCGAGGGAAG TTTACCTATG ACGCAGTGTA CTGCTGCAAT	1080
GAGCAGGCGT GCCATCACCG CTATGCTGAA TTATACGTGA TCGATGTCAA TATCAATATA	1140
TCATGTGAAA CTGACGGGTA CTTAACTAAA ATGACTTGCA GATGGTCACC CAGCACAATC	1200
CAATCACTAG TGGGAAGCAC TGTGCAGCTG AGGTATCACA GGCGCAGCCT GTATTGTCCT	1260
GATAGTCCAT CTATTCATCC TACGTCTGAG CCCAAAACT GCGTCTTACA GAGAGACGGC	1320
TTTTATGAAT GTGTTTTTCCA GCCAATCTTT CTATTATCTG GCTATACAAT GTGGATCAGG	1380
ATCAACCATT CTTTAGGTTT ACTTGACTCG CCACCAACGT GTGTCCTTCC TGAATCCGTA	1440
GTAAAACCAC TACCTCCATC TAACGTAAAA GCAGAGATTA CTGTAAACAC TGGATTATTG	1500
AAAGTATCTT GGGAAAAGCC AGTCTTTCCG GAGAATAACC TTCAATTCCA GATTTCATAT	1560

GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG	1620
TCTGCCAGCC TGCTGGTGTG AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG	1680
CGGTTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCATG	1740
GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT	1800
AAAAAGGAGA GAAATGTCAC CTTGCTTTGG AAGCCCCTGA CGAAAAATGA CTCACTGTGT	1860
AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCACACA ATGGGACGTG GTCAGAAGAT	1920
GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT	1980
CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC	2040
ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC	2100
ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG	2160
AAGATCCTTA ATGAAGATGA TGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG	2220
TTTTATATCC ACGATAATTT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA	2280
TTTATGGAAG GAGTTGGAAG ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC	2340
AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTT CTCTTGTGTC	2400
CTACTGCTCG GAACACTGTT AATTTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT	2460
GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC	2520
ACTCTTTGA	2529

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 842 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe

1		5						10					15			
Gln	Ala	Leu	Ser	Pro	Cys	Arg	Ile	Ser	Thr	Ser	Leu	Xaa	Leu	Val	Pro	
		20						25					30			
Asn	Ser	Ala	Arg	Gly	Cys	Phe	Gly	Asn	Glu	Gln	Gly	Gln	Asn	Cys	Ser	
		35					40					45				
Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	Ser	Val	Val	Lys	
	50					55					60					
Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	Ile	Glu	Cys	Trp	
65					70				75						80	
Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	Glu	Pro	Leu	Pro	
				85					90					95		
Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	Leu	Leu	Tyr	Asp	
			100					105						110		
Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	Leu	Lys	Asp	Ser	
		115					120						125			
Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	Cys	Glu	Cys	His	
	130					135					140					
Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu	
145					150					155					160	
Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	Leu	Met	Ser	Leu	
				165					170					175		
Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	Gly	Leu	His	Met	
			180					185					190			
Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	Asp	Ser	Gln	Thr	
	195						200					205				
Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	Leu	Glu	Asn	Ser	
	210					215					220					
Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	Thr	Ser	Leu	Leu	
225					230					235					240	
Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	Gln	Val	Arg	Ser	
				245					250					255		
Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	Ser	Ser	Pro	Gln	
		260						265					270			
Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	Lys	Ile	Leu	Thr	
		275					280					285				
Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	Lys	Asn	Glu	Asn	
	290					295					300					
Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	Asn	Leu	Ala	Glu	
305					310					315					320	

Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
 325 330 335
 Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
 340 345 350
 Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
 355 360 365
 Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
 370 375 380
 Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
 385 390 395 400
 Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
 405 410 415
 Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
 420 425 430
 Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
 435 440 445
 Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
 450 455 460
 Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
 465 470 475 480
 Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
 485 490 495
 Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
 500 505 510
 Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
 515 520 525
 Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
 530 535 540
 Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg
 545 550 555 560
 Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr
 565 570 575
 Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
 580 585 590
 Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
 595 600 605
 Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
 610 615 620

Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	625	630	635	640
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	645	650	655	
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	660	665	670	
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	675	680	685	
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	690	695	700	
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	705	710	715	720
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	725	730	735	
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	740	745	750	
Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	755	760	765	
Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	770	775	780	
Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	785	790	795	800
Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	805	810	815	
Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	820	825	830	
Leu	Asn	Phe	Gln	Lys	Arg	Thr	Asp	Thr	Leu							835	840		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTTG GAANTGAGTC CGAAGAGTCT	60
GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG	120
GATGTAGGCT AGCAGTTATT TCATTAGTAT ATGTCTATTT TAGAATGGGA AGAATTAGGA	180
AGATGAATGG AGCCTGTGTC TTTCACTACT CTCCCAGGAG GTTCCAGAAT AGCNAAAGTG	240
TCAGCCAGAA TTCTTGAAGT CATAGACTGG AGTTAGAGAT GAACATAAGC TCATGTTAAG	300
CCTGGGTAC TTCTTATCAT CCTTAATTTT GAAAGCTAAG AGGGCCTAAC CATCAAGAAC	360
GTCCTGGAGG AAAGAATGTT TTTAACGCCA TTATTCAGTC AAAGAAATTA AGACTTGAGA	420
GAAATGCTCA TTTCTTCTCT CATGATGGCT CCTTACACCT TACTTCTACC GTACGATCCA	480
TGNGGCCCTA CCCACGCAGG ATACATGCAT CTATATGAGA GTGTCTNCCC CTTCTAACTC	540
AGAGACTCTT GTTCTAGTCT GTGNTATAAA ATTCAGCTTG TGGAAGCTTT CTGAGGGGTT	600
GGCAGCATT C AATTTTACCT GCAATAGGTA AAGGTAATCT TTTGGGAAGT GAAGAGTGTT	660
ATTAGACATT TCAGAAAGAA CAAACAGGAT TGGGGCTGCT ATGTGTTCTA CACAGGAATC	720
TTCCATAACA CAGAATAATT TATGTAGATA GAGACAAGAT GGAAATGCCC AGGGCCCCAA	780
AATAGCCGCT GTTATTTGTT AACCTTCAAG GTTTTCTGTT TGTATCTG TTTCTTGCGC	840
AGGATCATCT TCCAAGCACA TCCTGGGGGA ACAGTGGCAG AGTCACTCGA GTTCATGAAA	900
CTATGGTGAC ATCTGAGCTT CCTTG GTTCT TCACAGAACA TAAGCAGTTC CTTTGCTTGC	960
TTGTTAGATG AGAAACTTC CTTGTCAGTC TGTCTCTACG ACTAGAATGG AAAGCCTTAC	1020
TACTTCCTAT GTATTCTTAA TATTTCAAAT GTCCTAATTA TGTTTGGCTT CTCTGTCTTT	1080
AAGGGATTTA GTCTCTGGAT TTGAAGAAAT AAATAAATAA ATAAAGGAAA ACTAATTTTC	1140
TCGTGCCGGA TGA CTGCTAG CTGAGCTCAG GCCTACTGCA TTCTACATTT CGACTCTCTC	1200
CCTCTTCCCC AGTGCTTTAG CACTGGACTG GGCAGTNCCT GGCCTGGTCT AACTCCTGTT	1260
TCCTGGTGGG AATGTATAAT AAGAACTCCA TGAGTTCTGG TATAAACACT GTGGTCTGTG	1320
TGCTAATTAA ATCTNGTGTT TCCTACAGCC CCTGACGAAA AATGACTCAC TGTGTAGTGT	1380
GAGGAGGTAC GTGGTGAAGC ATCGTACTGC CCACAATGGG ACGTGGTCAG AAGATGTGGG	1440
AAATCGGACC AATCTCACTT TCCTGTGGAC AGAACCAGCG CACACTGTTA CAGTTCTGGC	1500
TGTCAATTCC CTCGGCGCTT CCCTTG TGAA TTTTAACCTT ACCTTCTCAT GGCCCATGAG	1560

TAAAGTGAGT GCTGTGGAGT CACTCAGTGC TTATCCCCTG AGCAGCAGCT GTGTCATCCT	1620
TTCTTGACAC CTGTCACCTG ATGATTATAG TCTGTTATAT CTGGTTATTG AATGGAAGAT	1680
CCTTAATGAA GATGATGGAA TGAAGTGGCT TAGAATTCCC TCGAATGTTA AAAAGTTTTA	1740
TATCCACGAT AATTTTATTC CCATCGAGAA ATATCAGTTT AGTCTTTACC CAGTATTTAT	1800
GGAAGGAGTT GGAAAACCAA AGATAATTAA TGGTTTCACC AAAGATGCTA TCGACAAGCA	1860
GCAGAATGAC GCAGGGCTGT ATGTCATTGT ACCCATAATT ATTTCTCTT GTGTCCTACT	1920
GCTCGGAACA CTGTTAATTT CACACCAGAG AATGAAAAAG TTGTTTTGGG ACGATGTTCC	1980
AAACCCCAAG AATTGTTCTT GGGCACAAGG ACTGAATTTT CAAAAGCCTG AAACATTNGA	2040
GCATCTTTTT ACCAAGCATG CAGAATCAGT GATATTTGGT CCTCTTCTTC TGGAGCCTGA	2100
ACCCATTTCA GAAGAAATCA GTGTCGATAC AGCTTGGAAG AATAAAGATG AGATGGTCCC	2160
AGCAGCTATG GTCTCCCTNC TNNGGACCAC ACCAGACCCT GAAAGCAGTT CTATTTGTNT	2220
TAGTGACCAG TGTAACAGTG CTAACTTCTC TGGGTCTCAG AGCACCCAGG TAACCTGTGA	2280
GGATGAGTGT CAGAGACAAC CCTCAGTTAA ATATGCAACT CTGGTCAGCA ACGATAAACT	2340
AGTGGAAGT GATGAAGAGC AAGGGTTTAT CCATAGTCCT GTCAGCAACT GCATCTCCAG	2400
TAATCATTC CCACTGAGGC AGTCTTTCTC TAGCAGCTCC TGGGAGACAG AGGCCAGAC	2460
ATTTTCTCTT TTATCAGACC AGCAACCCAC CATGATTTCA CCACAACCTT CATTCTCGGG	2520
GTTGGATGAG CTTTTGGAAC TGGAGGGAAG TTTTCCTGAA GAAAATCACA GGGAGNAGTC	2580
TGTCTGTTAT CTAGGAGTCA CCTCCGTCCN CAGAAGAGAG AGTGGTGTGC TTTTGACTGG	2640
TGAGGCAGGA ATCCTGTGCA CATTCCCAGC CCAGTGTCTG TTCAGTGACA TCAGGATCCT	2700
CCAGGAGAGA TGCTCACACT TTGTAGAAAA TAATTTGAGT TTAGGGACCT CTGGTGAGAA	2760
CTTTGGTCCT AACATGCCCC AATTCCAAAC CTGTTCCACG CACAGTCACA AGATAATGGA	2820
GAATAAGATG TGTGACTTAA CTGTGTAA	2848

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Ile	Lys	Glu	
1				5					10					15		
Asn	Phe	Ser	Arg	Ala	Gly	Leu	Leu	Ala	Glu	Leu	Arg	Pro	Thr	Ala	Phe	
			20					25					30			
Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala	Leu	Asp	Trp	
		35					40					45				
Ala	Val	Pro	Gly	Leu	Val	Leu	Leu	Phe	Pro	Gly	Gly	Asn	Val	Glu	Leu	
	50					55					60					
His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu	Cys	Ala	Asn	Ile	Xaa	Cys	
65					70					75					80	
Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	
				85					90					95		
Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	
			100					105					110			
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	
		115					120					125				
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	
	130					135					140					
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	
145					150					155					160	
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	
				165					170					175		
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	
			180					185					190			
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	
		195					200					205				
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	
	210					215					220					
Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	
225					230					235					240	
Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	
				245					250					255		
Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	
			260					265						270		

Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	275	280	285
Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	290	295	300
Leu	Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	305	310	315
Ala	Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	325	330	335
Ser	Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	340	345	350
Val	Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	355	360	365
Ser	Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	370	375	380
Gly	Ser	Gln	Ser	Thr	Gln	Val	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro	385	390	395
Ser	Val	Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr	405	410	415
Asp	Glu	Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser	420	425	430
Ser	Asn	His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu	435	440	445
Thr	Glu	Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met	450	455	460
Ile	Ser	Pro	Gln	Leu	Ser	Phe	Ser	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu	465	470	475
Glu	Gly	Ser	Phe	Pro	Glu	Glu	Asn	His	Arg	Glu	Lys	Ser	Val	Cys	Tyr	485	490	495
Leu	Gly	Val	Thr	Ser	Val	Asn	Arg	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr	500	505	510
Gly	Glu	Ala	Gly	Ile	Leu	Cys	Thr	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser	515	520	525
Asp	Ile	Arg	Ile	Leu	Gln	Glu	Arg	Cys	Ser	His	Phe	Val	Glu	Asn	Asn	530	535	540
Leu	Ser	Leu	Gly	Thr	Ser	Gly	Glu	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln	545	550	555
Phe	Gln	Thr	Cys	Ser	Thr	His	Ser	His	Lys	Ile	Met	Glu	Asn	Lys	Met	565	570	575

Cys Asp Phe Thr Val
580

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 961 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTTCCTGGT GGAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT	240
GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT	540
CCTTTCCTGG ACACTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT	720
TATGGAAGGA GTTGGAAGAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA	780
GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTTCT CTTGTGTCCT	840
ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT	900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA	960
A	961

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Xaa	Ile	Lys
1				5					10					15	
Glu	Asn	Xaa	Phe	Ser	Arg	Ala	Gly	Xaa	Leu	Leu	Ala	Glu	Leu	Arg	Pro
			20					25					30		
Thr	Ala	Phe	Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala
		35					40					45			
Leu	Asp	Trp	Ala	Val	Pro	Gly	Leu	Val	Xaa	Leu	Leu	Phe	Pro	Gly	Gly
	50					55					60				
Asn	Val	Xaa	Xaa	Glu	Leu	His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu
65					70				75					80	
Cys	Ala	Asn	Xaa	Ile	Xaa	Cys	Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp
				85					90					95	
Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His
			100					105					110		
Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe
		115					120					125			
Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser
	130					135					140				
Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met
145					150				155						160
Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser
				165					170					175	
Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu
			180					185					190		

Leu Tyr Leu Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met
 195 200 205
 Lys Trp Leu Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp
 210 215 220
 Asn Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe
 225 230 235 240
 Met Glu Gly Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp
 245 250 255
 Ala Ile Asp Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro
 260 265 270
 Ile Ile Ile Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser
 275 280 285
 His Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys
 290 295 300
 Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe Gln Lys Val Thr Val
 305 310 315

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCTT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAAGTCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT	360

CGCCAGCTAG	GTGTAAACTG	GGACATAGAG	TGCTGGATGA	AAGGGGACTT	GACATTATTC	420
ATCTGTCATA	TGGAGCCATT	ACCTAAGAAC	CCCTTCAAGA	ATTATGACTC	TAAGGTCCAT	480
CTTTTATATG	ATCTGCCTGA	AGTCATAGAT	GATTTCGCCTC	TGCCCCCACT	GAAAGACAGC	540
TTTCAGACTG	TCCAATGCAA	CTGCAGTCTT	CGGGGATGTG	AATGTCATGT	GCCGGTACCC	600
AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTTGTTG	TGAAACCCGA	TCCACCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTTAAAGA	TTTCTTGGA	CAGCCAAACA	780
ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGACTION	960
AGTTCACCTC	AAGTCTTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTTGGAT	CGAATGCTTC	TTTTCATTCG	ATCTACAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTTGGTG	GAGGAATCTA	GCTGAGAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTION	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTION	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAACGCGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTION	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTCAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTTCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100

TTCCTGTGGA CAGAACCAGC GCACACTGTT ACAGTTCTGG CTGTCAATTC CCTCGGCGCT 2160
 TCCCTTGTGA ATTTTAACCT TACCTTCTCA TGGCCCATGA GTAAAGTGAG TGCTGTGGAG 2220
 TCACTCAGTG CTTATCCCCT GAGCAGCAGC TGTGTCATCC TTTCCTGGAC ACTGTCACCT 2280
 GATGATTATA GTCTGTTATA TCTGGTTATT GAATGGAAGA TCCTTAATGA AGATGATGGA 2340
 ATGAAGTGGC TTAGAATTCC CTCGAATGTT AAAAAGTTTT ATATCCACGA TAATTTTATT 2400
 CCCATCGAGA AATATCAGTT TAGTCTTTAC CCAGTATTTA TGGAAGGAGT TGGAAAACCA 2460
 AAGATAATTA ATGGTTTTCAC CAAAGATGCT ATCGACAAGC AGCAGAATGA CGCAGGGCTG 2520
 TATGTCATTG TACCCATAAT TATTTCTCT TGTGTCCTAC TGCTCGGAAC ACTGTTAATT 2580
 TCACACCAGA GAATGAAAAA GTTGTTTTGG GACGATGTTC CAAACCCCAA GAATTGTTCC 2640
 TGGGCACAAG GACTGAATTT CCAAAGGAT ATATCTTTAC ATGAAGTTTT TATTTTCAGA 2700
 TAG 2703

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu
1				5					10					15	
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys
			20					25					30		
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu
			35				40					45			
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser
			50			55					60				
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro

65					70					75					80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly
				85					90					95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala
			100					105					110		
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp
		115					120					125			
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met
	130					135					140				
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His
145					150					155					160
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro
				165					170					175	
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly
			180					185						190	
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu
		195					200					205			
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro
	210					215					220				
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu
225					230					235					240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp
			245						250					255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr
			260					265					270		
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala
		275					280					285			
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val
	290					295					300				
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp
305					310					315					320
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro
				325					330					335	
Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr
			340					345					350		
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg
		355					360					365			
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp
		370				375						380			

Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
 385 390 395 400
 Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
 405 410 415
 His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
 420 425 430
 Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
 435 440 445
 Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
 450 455 460
 His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
 465 470 475 480
 Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
 485 490 495
 Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
 500 505 510
 Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
 515 520 525
 Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
 530 535 540
 Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
 545 550 555 560
 Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
 565 570 575
 Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
 580 585 590
 Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
 595 600 605
 Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
 610 615 620
 Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
 625 630 635 640
 Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
 645 650 655
 Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
 660 665 670
 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
 675 680 685

Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
 690 695 700
 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720
 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735
 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
 740 745 750
 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765
 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780
 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
 785 790 795 800
 Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
 805 810 815
 Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
 820 825 830
 Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
 835 840 845
 Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
 850 855 860
 Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
 865 870 875 880
 Trp Ala Gln Gly Leu Asn Phe Gln Lys Asp Ile Ser Leu His Glu Val
 885 890 895
 Phe Ile Phe Arg
 900

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:

(B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGGAATCGT	TCTGCAAATC	CAGGTGTACA	CCTCTGAAGA	AAGATGATGT	GTCAGAAATT	60
CTATGTGGTT	TTGTTAACT	GGGAATTTCT	TTATGTGATA	GCTGCACTTA	ACCTGGCATA	120
TCCAATCTCT	CCCTGGAAAT	TTAAGTTGTT	TTGTGGACCA	CCGAACACAA	CCGATGACTC	180
CTTTCTCTCA	CCTGCTGGAG	CCCCAAACAA	TGCCTCGGCT	TTGAAGGGGG	CTTCTGAAGC	240
AATTGTTGAA	GCTAAATTTA	ATTCAAGTGG	TATCTACGTT	CCTGAGTTAT	CCAAAACAGT	300
CTTCCACTGT	TGCTTTGGGA	ATGAGCAAGG	TCAAACTGC	TCTGCACTCA	CAGACAACAC	360
TGAAGGGAAG	AACTGGCTT	CAGTAGTGAA	GGCTTCAGTT	TTTCGCCAGC	TAGGTGTAAA	420
CTGGGACATA	GAGTGCTGGA	TGAAAGGGGA	CTTGACATTA	TTCATCTGTC	ATATGGAGCC	480
ATTACCTAAG	AAACCCTTCA	AGAATTATGA	CTCTAAGGTC	CATCTTTTAT	ATGATCTGCC	540
TGAAGTCATA	GATGATTCGC	CTCTGCCCCC	ACTGAAAGAC	AGCTTTCAGA	CTGTCCAATG	600
CAACTGCAGT	CTTCGGGGAT	GTGAATGTCA	TGTGCCGGTA	CCCAGAGCCA	AACTCAACTA	660
CGCTCTTCTG	ATGTATTTGG	AAATCACATC	TGCCGGTGTG	AGTTTTTCAGT	CACCTCTGAT	720
GTCAGTGCAG	CCCATGCTTG	TTGTGAAACC	CGATCCACCC	TTAGGTTTGC	ATATGGAAGT	780
CACAGATGAT	GGTAATTTAA	AGATTTCTTG	GGACAGCCAA	ACAATGGCAC	CATTTCCGCT	840
TCAATATCAG	GTGAAATATT	TAGAGAATTC	TACAATTGTA	AGAGAGGCTG	CTGAAATTGT	900
CTCAGCTACA	TCTCTGCTGG	TAGACAGTGT	GCTTCCTGGA	TCTTCATATG	AGGTCCAGGT	960
GAGGAGCAAG	AGACTGGATG	GTTTCAGGAGT	CTGGAGTGAC	TGGAGTTCAC	CTCAAGTCTT	1020
TACCACACAA	GATGTTGTGT	ATTTTCCACC	CAAAATTCTG	ACTAGTGTTG	GATCGAATGC	1080
TTCTTTTCAT	TGCATCTACA	AAAACGAAAA	CCAGATTATC	TCCTCAAAAC	AGATAGTTTG	1140
GTGGAGGAAT	CTAGCTGAGA	AAATCCCTGA	GATACAGTAC	AGCATTGTGA	GTGACCGAGT	1200
TAGCAAAGTT	ACCTTCTCCA	ACCTGAAAGC	CACCAGACCT	CGAGGGAAGT	TTACCTATGA	1260
CGCAGTGATC	TGCTGCAATG	AGCAGGCGTG	CCATCACCGC	TATGCTGAAT	TATACGTGAT	1320
CGATGTCAAT	ATCAATATAT	CATGTGAAAC	TGACGGGTAC	TTAACTAAAA	TGACTTGCAG	1380
ATGGTCACCC	AGCACAATCC	AATCACTAGT	GGGAAGCACT	GTGCAGCTGA	GGTATCACAG	1440
GCGCAGCCTG	TATTGTCCTG	ATAGTCCATC	TATTCATCCT	ACGTCTGAGC	CCAAAACTG	1500
CGTCTTACAG	AGAGACGGCT	TTTATGAATG	TGTTTTCCAG	CCAATCTTTC	TATTATCTGG	1560

CTATACAATG TGGATCAGGA TCAACCATTG TTTAGGTTCA CTTGACTCGC CACCAACGTG	1620
TGTCCTTCCT GACTCCGTAG TAAAACCACT ACCTCCATCT AACGTAAAAG CAGAGATTAC	1680
TGTAAACACT GGATTATTGA AAGTATCTTG GGAAAAGCCA GTCTTTCCGG AGAATAACCT	1740
TCAATTCCAG ATTCGATATG GCTTAAGTGG AAAAGAAATA CAATGGAAGA CACATGAGGT	1800
ATTCGATGCA AAGTCAAAGT CTGCCAGCCT GCTGGTGTCA GACCTCTGTG CAGTCTATGT	1860
GGTCCAGGTT CGCTGCCGGC GGTTGGATGG ACTAGGATAT TGGAGTAATT GGAGCAGTCC	1920
AGCCTATACG CTTGTCATGG ATGTAAAAGT TCCTATGAGA GGGCCTGAAT TTTGGAGAAA	1980
AATGGATGGG GACGTTACTA AAAAGGAGAG AAATGTCACC TTGCTTTGGA AGCCCCTGAC	2040
GAAAAATGAC TCACTGTGTA GTGTGAGGAG GTACGTGGTG AAGCATCGTA CTGCCCACAA	2100
TGGGACGTGG TCAGAAGATG TGGGAAATCG GACCAATCTC ACTTTCCTGT GGACAGAACC	2160
AGCGCACACT GTTACAGTTC TGGCTGTCAA TTCCCTCGGC GCTTCCCTTG TGAATTTTAA	2220
CCTTACCTTC TCATGGCCCA TGAGTAAAGT GAGTGCTGTG GAGTCACTCA GTGCTTATCC	2280
CCTGAGCAGC AGCTGTGTCA TCCTTTCCTG GACACTGTCA CCTGATGATT ATAGTCTGTT	2340
ATATCTGGTT ATTGAATGGA AGATCCTTAA TGAAGATGAT GGAATGAAGT GGCTTAGAAT	2400
TCCCTCGAAT GTTAAAAAGT TTTATATCCA CGGTATGTGT ACTGTACTTT TCATGGATTA	2460
G	2461

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 805 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu
1				5					10					15	

Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys

20					25					30					
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu
		35						40				45			
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser
	50					55					60				
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro
65					70					75					80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly
				85					90					95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala
			100					105					110		
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp
		115					120					125			
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met
	130					135					140				
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His
145					150					155					160
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro
				165					170					175	
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly
			180					185					190		
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu
		195					200					205			
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro
	210					215					220				
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu
225					230					235					240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp
				245					250					255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr
			260					265					270		
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala
		275					280					285			
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val
	290					295					300				
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp
305					310					315					320
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro
				325					330					335	

Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
 340 345 350
 Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
 355 360 365
 Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
 370 375 380
 Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
 385 390 395 400
 Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
 405 410 415
 His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
 420 425 430
 Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
 435 440 445
 Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
 450 455 460
 His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
 465 470 475 480
 Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
 485 490 495
 Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
 500 505 510
 Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
 515 520 525
 Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
 530 535 540
 Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
 545 550 555 560
 Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
 565 570 575
 Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
 580 585 590
 Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
 595 600 605
 Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
 610 615 620
 Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
 625 630 635 640

Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
 645 650 655
 Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
 660 665 670
 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
 675 680 685
 Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
 690 695 700
 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720
 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735
 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
 740 745 750
 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765
 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780
 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Gly Met Cys Thr
 785 790 795 800
 Val Leu Phe Met Asp
 805

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Phe Gln Lys Arg Thr Asp Leu 8

1

5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	Ala	1	5	10	15
Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser	20	25	30	
Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val	35	40	45	
Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	Ser	50	55	60	
Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly	65	70	75	80
Ser	Gln	Ser	Thr	Gln	Val	Cys	Glu	Asp	Glu	Cys	Gln	Arg	Gln	Pro	Ser	85	90	95	
Val	Lys	Tyr	Ala	Thr	Leu	Val	Ser	Asn	Asp	Lys	Leu	Val	Glu	Thr	Asp	100	105	110	
Glu	Glu	Gln	Gly	Phe	Ile	His	Ser	Pro	Val	Ser	Asn	Cys	Ile	Ser	Ser	115	120	125	
Asn	His	Ser	Pro	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ser	Ser	Trp	Glu	Thr	130	135	140	
Glu	Ala	Gln	Thr	Phe	Phe	Leu	Leu	Ser	Asp	Gln	Gln	Pro	Thr	Met	Ile	145	150	155	160
Ser	Pro	Gln	Leu	Ser	Phe	Ser	Gly	Leu	Asp	Glu	Leu	Leu	Glu	Leu	Glu	165	170	175	

Gly	Ser	Phe	Pro	Glu	Glu	Asn	His	Arg	Glu	Lys	Ser	Val	Cys	Tyr	Leu
			180					185					190		
Gly	Val	Thr	Ser	Val	Asn	Arg	Arg	Glu	Ser	Gly	Val	Leu	Leu	Thr	Gly
		195					200					205			
Glu	Ala	Gly	Ile	Leu	Cys	Thr	Phe	Pro	Ala	Gln	Cys	Leu	Phe	Ser	Asp
	210					215					220				
Ile	Arg	Ile	Leu	Gln	Glu	Arg	Cys	Ser	His	Phe	Val	Glu	Asn	Asn	Leu
225				230						235					240
Ser	Leu	Gly	Thr	Ser	Gly	Glu	Asn	Phe	Gly	Pro	Tyr	Met	Pro	Gln	Phe
			245					250						255	
Gln	Thr	Cys	Ser	Thr	His	Ser	His	Lys	Ile	Met	Glu	Asn	Lys	Met	Cys
		260						265					270		
Asp	Phe	Thr	Val												
		275													

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn	Phe	Gln	Lys	Val	Thr	Val
1				5		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn	Phe	Gln	Lys	Asp	Ile	Ser	His	Glu	Val	Phe	Ile	Phe	Arg
1				5					10				

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe	Tyr	Ile	His	Gly	Met	Cys	Thr	Val	Leu	Phe	Met	Asp
1				5					10			

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
1 5 10 15

Ser Glu Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Arg Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn
 1 5 10 15

Cys Ser Trp

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA	60
CAGGAAAGTG AGATTGGTCC GATTTCCCAC ATCTTCTGAC CACGTCCCAT TGTGGGCAGT	120
ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT	166

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA	60
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TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCT	120
CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTATTGAA TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT	120
CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTTCATT TGATGTTTCAG	60
AAGTCAGCAA GGTTCTCATA TGTCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG	120
CTAACAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT	180
TAAAGATACG AG	192

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTT TCATCTAACA AGCAAGCAAA GGAAGTCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA	168

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC TGAAGTCATA GATGATTCGC	60
CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTGCGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG	180
NAATCACATC TGCCGGTGTG AGTTTTTCAGT CACCTCTGAT GTCAGTGCAG CCCATGCTTG	240
TTGTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTTTC GTGGTCCACA AAACAACCTA AATTTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA	180
AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTGCAG	240
AACGATTCCT	250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC

18

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG

22

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTCCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGC GCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCACTG

20